



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: DONNELLY, JOHN J.
DWARKI, VARAVANI J.
LIU, MARGARET A.
MONTGOMERY, DONNA L.
PARKER, SUEZANNE E.
SHIVER, JOHN W.
ULMER, JEFFREY B.
- (ii) TITLE OF THE INVENTION: NUCLEIC ACID PHARMACEUTICALS -
INFLUENZA MATRIX
- (iii) NUMBER OF SEQUENCES: 64
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
 - (B) STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
 - (C) CITY: RAHWAY
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 07065-0907
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/835,694
 - (B) FILING DATE: 16-April-2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/461,268
 - (B) FILING DATE: 05-June-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US94/02751
 - (B) FILING DATE: 14-March-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/089,985
 - (B) FILING DATE: 08-July-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/032,383
 - (B) FILING DATE: 18-March-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: HAND, J. MARK
 - (B) REGISTRATION NUMBER: 36,545
 - (C) REFERENCE/DOCKET NUMBER: 18972PCA
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 732-594-3905
 - (B) TELEFAX: 732-594-4720
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGTGCACCT CAAGCTGG

18

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCTTTGAGA ATGTTGCACA TTC

23

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTACAAGAT CTACCATGCT TCTAACCGAG GTC

33

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: YES
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCACATAGAT CTTCACTTGA ACCGTTGCAT CTGCAC

36

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTATATAAGC AGAGCTCGTT TAG

23

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: YES
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTAGCAAAGA TCTAAGGACG GTGACTGCAG

30

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTATGTGTCT GAAAATGAGC GTGGAGATTG GGCTCGCAC

39

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: YES

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCGAGCCC AATCTCCACG CTCATTTTCA GACACATAC

39

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: None

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Tyr Gln Arg Thr Arg Ala Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCGCGCGTTT	CGGTGATGAC	GGTGAAAACC	TCTGACACAT	GCAGTCCCG	GAGACGGTCA	60
CAGCTTGTCT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCG	TCAGGGCGCG	TCAGCGGGTG	120
TTGGCGGGTG	TCGGGGCTGG	CTTAACATATG	CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC	180
ACCATATGCG	GTGTGAAATA	CCGCACAGAT	GCGTAAGGAG	AAAATACCGC	ATCAGATTGG	240
CTATTGGCCA	TTGCATACGT	TGTATCCATA	TCATAATATG	TACATTTATA	TTGGCTCATG	300
TCCAACATTA	CCGCCATGTT	GACATTGATT	ATTGACTAGT	TATTAATAGT	AATCAATTAC	360

GGGGTCATTA	GTTCATAGCC	CATATATGGA	GTTCCGCGTT	ACATAACTTA	CGGTAAATGG	420
CCCGCCTGGC	TGACCGCCCA	ACGACCCCCG	CCCATTGACG	TCAATAATGA	CGTATGTTCC	480
CATAGTAACG	CCAATAGGGA	CTTTCCATTG	ACGTCAATGG	GTGGAGTATT	TACGGTAAAC	540
TGCCCCACTG	GCAGTACATC	AAGTGTATCA	TATGCCAAGT	ACGCCCCCTA	TTGACGTCAA	600
TGACGGTAAA	TGGCCCGCCT	GGCATTATGC	CCAGTACATG	ACCTTATGGG	ACTTTCCTAC	660
TTGGCAGTAC	ATCTACGTAT	TAGTCATCGC	TATTACCATG	GTGATGCGGT	TTTGGCAGTA	720
CATCAATGGG	CGTGGATAGC	GGTTTGACTC	ACGGGGATT	CCAAGTCTCC	ACCCCATTTGA	780
CGTCAATGGG	AGTTTGT	GGCACAAAA	TCAACGGGAC	TTTCCAAAAT	GTCGTAACAA	840
CTCCGCCCCA	TTGACGCAAA	TGGGCGGTAG	GCGTGTACGG	TGGGAGGTCT	ATATAAGCAG	900
AGCTCGTTTA	TTGAACCGTC	AGATCGCCTG	GAGACGCCAT	CCACGCTGTT	TTGACCTCCA	960
TAGAAGACAC	CGGGACCGAT	CCAGCCTCCG	CGGCCGGGAA	CGGTGCATTG	GAACGCGGAT	1020
TCCCCGTGCC	AAGAGTGACG	TAAGTACCGC	CTATAGAGTC	TATAGGCCCA	CCCCCTTGGC	1080
TTCTTATGCA	TGCTATACTG	TTTTTGGCTT	GGGGTCTATA	CACCCCGCT	TCCTCATGTT	1140
ATAGGTGATG	GTATAGCTTA	GCCTATAGGT	GTGGGTATT	GACCATTTAT	GACCATCCCC	1200
CTATTGGTGA	CGATACTTTC	CATTACTAAT	CCATAACATG	GCTCTTTGCC	ACAACCTCTCT	1260
TTATTGGCTA	TATGCCAATA	CACTGTCCCT	CAGAGACTGA	CACGGACTCT	GTATTTTTTAC	1320
AGGATGGGGT	CTCATTTTAT	ATTTACAAAT	TCACATATAC	AACACCACCG	TCCCCAGTGC	1380
CCGCAGTTTT	TATTAAACAT	AACGTGGGAT	CTCCACGCGA	ATCTCGGGTA	CGTGTTCCGG	1440
ACATGGGCTC	TTCTCCGGTA	GCGGCGGAGC	TTCTACATCC	GAGCCCTGCT	CCCATGCCTC	1500
CAGCGACTCA	TGGTCGCTCG	GCAGCTCCTT	GCTCCTAACA	GTGGAGGCCA	GACTTAGGCA	1560
CAGCACGATG	CCCACCACCA	CCAGTGTGCC	GCACAAGGCC	GTGGCGGTAG	GGTATGTGTC	1620
TGAAAATGAG	CTCGGGGAGC	GGGCTTGCAC	CGCTGACGCA	TTTGAAGAC	TTAAGGCAGC	1680
GGCAGAAAG	GATGCAGGCA	GCTGAGTTGT	TGTGTTCTGA	TAAGAGTCAG	AGGTAACTCC	1740
CGTTGCGGTG	CTGTTAACGG	TGGAGGGCAG	TGTAGTCTGA	GCAGTACTCG	TTGCTGCCGC	1800
GCGCGCCACC	AGACATAATA	GCTGACAGAC	TAACAGACTG	TTCTTTTCCA	TGGGTCTTTT	1860
CTGCAGTCAC	CGTCTTAGA	TCTGCTGTGC	CTTCTAGTTG	CCAGCCATCT	GTGTGTTGCC	1920
CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	GTGCCACTCC	CACGTCTCCT	TCCTAATAAA	1980
ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	GGTGTCATTC	TATTCTGGGG	GGTGGGGTGG	2040
GGCAGCACAG	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	2100
GCTCTATGGG	TACCCAGGTG	CTGAAGAAAT	GACCCGGTTC	CTCCTGGGCC	AGAAAGAAGC	2160
AGGCACATGC	CCTTCTCTGT	GACACACCCCT	GTCCACGCC	CTGGTTCTTA	GTTCCAGCCC	2220
CACTCATAGG	ACACTCATAG	CTCAGGAGGG	CTCCGCCTTC	AATCCCACCC	GCTAAAGTCA	2280
TTGGAGCGGT	CTCTCCCTCC	CTCATCAGCC	CACCAAACCA	AACCTAGCCT	CCAAGAGTGG	2340
GAAGAAATTA	AAGCAAGATA	GGCTATTAAG	TGCAGAGGGA	GAGAAAATGC	CTCCAACATG	2400
TGAGGAAGTA	ATGAGAGAAA	TCATAGAAAT	TCTTCCGCTT	CCTCGCTCAC	TGACTCGCTG	2460
CGCTCGGTG	TTCCGGCTGCG	GCGAGCGGTA	TCAGTCTACT	CAAAGGCGGT	AATACGGTTA	2520
TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC	2580
AGGAACCGTA	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	CCCTGACGAG	2640
CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	CGACAGGACT	ATAAAGATAC	2700
CAGGCGTTTC	CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	GCCGCTTACC	2760
GGATACCTGT	CCGCTTTCT	CCCTTCGGGA	AGCGTGGCGC	TTTCTCAATG	CTCACGCTGT	2820
AGGTATCTGA	GTTCCGGTGTA	GGTCGTTGCG	TCCAAGCTGG	GCTGTGTGCA	CGAACCCCCC	2880
GTTACAGCCG	ACCGCTGCGC	CTTATCCGGT	AACATATCGTC	TTGAGTCCAA	CCCGGTAAGA	2940
CACGACTTAT	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	GAGGTATGTA	3000
GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	CCTAACTACG	GCTACACTAG	AAGGACAGTA	3060
TTTGGTATCT	GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	TAGCTCTTGA	3120
TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTT	TTTGCAAGCA	GCAGATTACG	3180
CGCAGAAAAA	AAGGATCTCA	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC	TGACGCTCAG	3240
TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	TATCAAAAAG	GATCTTCACC	3300
TAGATCTCTT	TAAATTAAAA	ATGAAGTTTT	AAATCAATCT	AAAGTATATA	TGAGTAAACT	3360
TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	TCTCAGCGAT	CTGTCTATTT	3420
CGTTCATCCA	TAGTTGCCTG	ACTCCCCGTC	GTGTAGATAA	CTACGATACG	GGAGGGCTTA	3480
CCATCTGGCC	CCAGTGCTGC	AATGATACCG	CGAGACCCAC	GCTCACCGGC	TCCAGATTTA	3540
TCAGCAATAA	ACCAGCCAGC	CGGAAGGGCC	GAGCGCAGAA	GTGGTCCTGC	AACTTTATCC	3600
GCCTCCATCC	AGTCTATTAA	TTGTTGCCGG	GAAGCTAGAG	TAAGTAGTTC	GCCAGTTAAT	3660
AGTTTGCGCA	ACGTTGTTGC	CATTGCTACA	GGCATCGTGG	TGTCACGCTC	GTCGTTTGGT	3720
ATGGCTTCAT	TCAGTCCCGG	TTCCCAACGA	TCAAGGCGAG	TTACATGATC	CCCCATGTTG	3780
TGCAAAAAAG	CGGTTAGCTC	CTTCGGTCTT	CCGATCGTTG	TCAGAAGTAA	GTTGGCCGCA	3840
GTGTTATCAC	TCATGGTTAT	GGCAGCACTG	CATAATTCTC	TTACTGTTCAT	CCCATCCGTA	3900
AGATGCTTTT	CTGTGACTGG	TGAGTACTCA	ACCAAGTCAT	TCTGAGAATA	GTGTATGCGG	3960
CGACCGAGTT	GCTCTTGCCC	GGCGTCAATA	CGGGATAATA	CCGCGCCACA	TAGCAGAACT	4020
TTAAAAGTGC	TCATCATTTG	AAAACGTTCT	TGGGGCGGAA	AACTCTCAAG	GATCTTACCG	4080

CTGTTGAGAT	CCAGTTCGAT	GTAACCCACT	CGTGACCCCA	ACTGATCTTC	AGCATCTTTT	4140
ACTTTCACCA	GCGTTTCTGG	GTGAGCAAAA	ACAGGAAGGC	AAAATGCCGC	AAAAAAGGGA	4200
ATAAGGGCGA	CACGGAAATG	TTGAATACTC	ATACTCTTCC	TTTTTCAATA	TTATTGAAGC	4260
ATTTATCAGG	GTTATTGTCT	CATGAGCGGA	TACATATTTG	AATGTATTTA	GAAAAATAAA	4320
CAAATAGGGG	TTCCGCGCAC	ATTTCCCCGA	AAAGTGCCAC	CTGACGTCTA	AGAAACCATT	4380
ATTATCATGA	CATTAAACCTA	TAAAAATAGG	CGTATCACGA	GGCCCTTTCG	TC	4432

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTGGCTATT	GGCCATTGCA	TACGTTGTAT	CCATATCATA	ATATGTACAT	TTATATTGGC	60
TCATGTCCAA	CATTACCGCC	ATGTTGACAT	TGATTATTGA	CTAGTTATTA	ATAGTAATCA	120
ATTACGGGGT	CATTAGTTCA	TAGCCCATAT	ATGGAGTTCC	GCGTTACATA	ACTTACGGTA	180
AATGGCCCCG	CTGGCTGACC	GCCCAACGAC	CCCCGCCCAT	TGACGTCAAT	AATGACGTAT	240
GTTCCCATAG	TAACGCCAAT	AGGGACTTTC	CATTGACGTC	AATGGGTGGA	GTATTTACGG	300
TAAACTGCCC	ACTTGGCAGT	ACATCAAGTG	TATCATATGC	CAAGTACGCC	CCCTATTGAC	360
GTCAATGACG	GTAATGGCC	CGCCTGGCAT	TATGCCCAGT	ACATGACCTT	ATGGGACTTT	420
CCTACTTGGC	AGTACATCTA	CGTATTAGTC	ATCGCTATTA	CCATGGTGAT	GCGGTTTTGG	480
CAGTACATCA	ATGGGCGTGG	ATAGCGGTTT	GACTCACGGG	GATTTCCAAG	TCTCCACCCC	540
ATTGACGTCA	ATGGGAGTTT	GTTTGGGCAC	CAAAATCAAC	GGGACTTTCC	AAAATGTCGT	600
AACAACCTCG	CCCCATTGAC	GCAAATGGGC	GGTAGGCGTG	TACGGTGGGA	GGTCTATATA	660
AGCAGAGCTC	GTTTAGTGAA	CCGTCAGATC	GCCTGGAGAC	GCCATCCACG	CTGTTTTGAC	720
CTCCATAGAA	GACACCGGGA	CCGATCCAGC	CTCCGCGGGC	GGGAACGGTG	CATTGGAACG	780
CGGATTCCCC	GATGCCAAGAG	TGACGTAAAGT	ACCGCCTATA	GAGTCTATAG	GCCCACCCCC	840
TTGGCTTCTT	ATGCATGCTA	TACTGTTTTT	GGCTTGGGGT	CTATACACCC	CCGCTTCCCTC	900
ATGTTATAGG	TGATGGTATA	GCTTAGCCTA	TAGGTGTGGG	TTATTGACCA	TTATTGACCA	960
CTCCCCTATT	GGTGACGATA	CTTTCCATTA	CTAATCCATA	ACATGGCTCT	TTGCCACAAC	1020
TCTCTTTATT	GGCTATATGC	CAATACACTG	TCCTTCAGAG	ACTGACACGG	ACTCTGTATT	1080
TTTACAGGAT	GGGGTCTCAT	TTATTATTTA	CAAATTCACA	TATACAACAC	CACCGTCCCC	1140
AGTGCCCGCA	GTTTTTTATTA	AACATAACGT	GGGATCTCCA	CGCGAATCTC	GGGTACGTGT	1200
TCCGGACATG	GGCTCTTCTC	CGGTAGCGGC	GGAGCTTCTA	CATCCGAGCC	CTGCTCCCAT	1260
GCCTCCAGCG	ACTCATGGTC	GCTCGGCAGC	TCCTTGCTCC	TAACAGTGGA	GGCCAGACTT	1320
AGGCACAGCA	CGATGCCCAC	CACCACCAGT	GTGCCGCACA	AGGCCGTGGC	GGTAGGGTAT	1380
GTGTCTGAAA	ATGAGCTCGG	GGAGCGGGCT	TGCACCGCTG	ACGCATTTGG	AAGACTTAAG	1440
GCAGCGGCAG	AAGAAGATGC	AGGCAGCTGA	GTTGTTGTGT	TCTGATAAGA	GTCAGAGGTA	1500
ACTCCCGTTG	CGGTGCTGTT	AACGGTGGAG	GGCAGTGTAG	TCTGAGCAGT	ACTCGTTGCT	1560
GCCGCGCGCG	CCACCAGACA	TAATAGCTGA	CAGACTAACA	GACTGTTTCT	TTCCATGGGT	1620
CTTTTCTGCA	GTCACCGTCC	TTAGATCTGC	TGTGCCTTCT	AGTTGCCAGC	CATCTGTTGT	1680
TTGCCCCCTC	CCCGTGCCCT	CCTTGACCCT	GGAAGGTGCC	ACTCCCACTG	TCCTTTCCCTA	1740
ATAAAATGAG	GAAATTGCAT	CGCATTGTCT	GAGTAGGTGT	CATTCTATTTC	TGGGGGGTGG	1800
GGTGGGGCAG	CACAGCAAGG	GGGAGGATTG	GGAAGACAAT	AGCAGGCATG	CTGGGGATGC	1860
GGTGGGCTCT	ATGGGTACCC	AGGTGCTGAA	GAATTGACCC	GGTTCCTCCT	GGGCCAGAAA	1920
GAAGCAGGCA	CATCCCCCTC	TCTGTGACAC	ACCCTGTCCA	CGCCCCTGGT	TCTTAGTTCC	1980
AGCCCCACTC	ATAGGACACT	CATAGCTCAG	GAGGGCTCCG	CCTTCAATCC	CACCCGCTAA	2040
AGTACTTGGA	GCGGTCTCTC	CCTCCCTCAT	CAGCCCACCA	AACCAAACCT	AGCCTCCAAG	2100
AGTGGGAAGA	AATTAAAGCA	AGATAGGCTA	TTAAGTGCAG	AGGGAGAGAA	AATGCCTCCA	2160
ACATGTGAGG	AAGTAATGAG	AGAAATCATA	GAATTC			2196

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCACCGTCC TTAGATCAAT TCCAGCAAAA GCAGGGTAGA TAATCACTCA CTGAGTGACA
TCAAAATCAT G

60
71

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACCGTCCTTA GATCAGCTTG GCAAAAGCAG GCAAACCATT TGAATGGATG TCAATCCGAC
CTTACTTTTC TAAAAGTGC CAGCACAAA TGCTATAAGC ACAACTTTCC CTTATAC

60
117

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTCACCGTCC TTAGATCAAT TCCAGCAAAA GCAGGGTGAC AAAACATAA TGGATCCAAA
CACTGTGTCA AGCTTTCAGG TAGATTGCTT TCTTTGGCAT GTCCGCAAC GAGTTGCAGA
CCAAGAATA GGTGAT

60
120
136

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCTGCAGTCA	CCGTCCTTAG	ATCAGCTTGG	AGCAAAAGCA	GGGGAAAATA	AAAACAACCA	60
AAATGAAGGC	AAACCTACTG	GTCCTGTAA	GTGCACTTGC	AGCTGCAGAT	GCAGACACAA	120
TATGTATAGG	CTACCATGCG	AACAATTCAA	CC			152

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTTCTGCAG	TCACCGTCCT	TAGATCCCGA	ATTCCAGCAA	AAGCAGGTCA	ATTATATTCA	60
ATATGGAAAG	AATAAAAGAA	CTAAGAAATC	TAATGTCGCA	GTCTGCCACC	CCGGAGATAC	120
TCACAAAAC	CACCGTGGAC	CATATGGCCA	TAATCAAGAA	GT		162

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCACCGTCC	TTAGATCTAC	CATGAGTCTT	CTAACCGAGG	TCGAAACGTA	CGTACTCTCT	60
ATCATCCCGT	CAGGCCCCCT	CAAAGCCGAG	ATCGCACAGA	GACTTGAAGA	GTTGACGGAA	120
GA						122

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4864 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCGCGCGTTT	CGGTGATGAC	GGTGAAAACC	TCTGACACAT	GCAGCTCCCC	GAGACGGTCA	60
CAGCTTGTCT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCC	TCAGGGCGCG	TCAGCGGGTG	120
TTGGCGGGTG	TCGGGGCTGG	CTTAACATATG	CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC	180
ACCATATGCG	GTGTGAAATA	CCGCACAGAT	GCGTAAGGAG	AAAATACCGC	ATCAGATTGG	240
CTATTGGCCA	TTGCATACGT	TGTATCCATA	TCATAATATG	TACATTTATA	TTGGCTCATG	300
TCCAACATTA	CCGCCATGTT	GACATTGATT	ATTGACTAGT	TATTAATAGT	AATCAATTAC	360
GGGGTCATTA	GTTCATAGCC	CATATATGGA	GTTCCGCGTT	ACATAACTTA	CGGTAAATGG	420
CCCGCCTGGC	TGACCGCCCA	ACGACCCCCG	CCCATTGACG	TCAATAATGA	CGTATGTTCC	480
CATAGTAACG	CCAATAGGGA	CTTTCCATTG	ACGTCAATGG	GTGGAGTATT	TACGGTAAAC	540
TGCCCCACTTG	GCAGTACATC	AAGTGTATCA	TATGCCAAGT	ACGCCCCCTA	TTGACGTCAA	600
TGACGGTAAA	TGGCCCGCCT	GGCATTATGC	CCAGTACATG	ACCTTATGGG	ACTTTCCTAC	660
TTGGCAGTAC	ATCTACGTAT	TAGTCATCGC	TATTACCATG	GTGATGCGGT	TTTGGCAGTA	720
CATCAATGGG	CGTGGATAGC	GGTTTGACTC	ACGGGGATTT	CCAAGTCTCC	ACCCCATTTGA	780
CGTCAATGGG	AGTTTGTTTT	GGCACCAAAA	TCAACGGGAC	TTTCCAAAAT	GTCGTAAACA	840
CTCCGCCCCA	TTGACGCAAA	TGGGCGGTAG	GCGTGTACGG	TGGGAGGTCT	ATATAAGCAG	900
AGCTCGTTTA	GTGAACCGTC	AGATCGCCTG	GAGACGCCAT	CCACGCTGTT	TTGACCTCCA	960
TAGAAGACAC	CGGGACCGAT	CCAGCCTCCG	CGGCCGGGAA	CGGTGCATTG	GAACGCGGAT	1020
TCCCCGTGCC	AAGAGTGACG	TAAGTACCGC	CTATAGAGTC	TATAGGCCCA	CCCCCTTGGC	1080
TTCTTATGCA	TGCTATACTG	TTTTTGGCTT	GGGGTCTATA	CACCCCGCT	TCCTCATGTT	1140
ATAGGTGATG	GTATAGCTTA	GCCTATAGGT	GTGGGTATT	GACCATTATT	GACCACTCCC	1200
CTATTGGTGA	CGATACTTTC	CATTACTAAT	CCATAACATG	GCTCTTTGCC	ACAACCTCTCT	1260
TTATTGGCTA	TATGCCAATA	CACTGTCTCT	CAGAGACTGA	CACGGACTCT	GTATTTTTTAC	1320
AGGATGGGGT	CTCATTTATT	ATTTACAAAT	TCACATATAC	AACACCACCG	TCCCCAGTGC	1380
CCGCAGTTTT	TATTAACAT	AACGTGGGAT	CTCCACGCGA	ATCTCGGGTA	CGTGTTCGGG	1440
ACATGGGCTC	TTCTCCGGTA	GCGGCGGAGC	TTCTACATCC	GAGCCCTGCT	CCCATGCCTC	1500
CAGCGACTCA	TGGTCGCTCG	GCAGCTCCTT	GCTCCTAACA	GTGGAGGCCA	GACTTAGGCA	1560
CAGCAGATG	CCCACCACCA	CCAGTGTGCC	GCACAAGGCC	GTGGCGGTAG	GGTATGTGTC	1620
TGAAAATGAG	CTCGGGGAGC	GGGCTTGCAC	CGCTGACGCA	TTTGGAAGAC	TTAAGGCAGC	1680
GGCAGAAGAA	GATGCAGGCA	GCTGAGTTGT	TGTGTTCTGA	TAAGAGTCAG	AGGTAACCTC	1740
CGTTGCGGTG	CTGTTAACGG	TGGAGGGCAG	TGTAGTCTGA	GCAGTACTCG	TTGCTGCCCG	1800
GCGCGCCACC	AGACATAATA	GCTGACAGAC	TAACAGACTG	TTCTTTTCCA	TGGGTCTTTT	1860
CTGCACTCAC	CGTCTCTAGA	TCTGCTGTGC	CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	1920
CCTCCCCCTG	GCCTTCTCTG	ACCTTGGAAG	GTGCCACTCC	CACGTCTCTT	TCCTAATAAA	1980
ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	GGTGTCTATC	TATTCTGGGG	GGTGGGGTGG	2040
GGCAGCACAG	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	2100
GCTCTATGGG	TACCCAGGTG	CTGAAGAAAT	GACCCGGTTC	CTCTGGGGCC	AGAAGAAGC	2160
AGGCACATCC	CCTTCTCTGT	GACACACCTT	GTCCACGCCC	CTGGTTCTTA	GTTCCAGCCC	2220
CACTCATAGG	ACACTCATAG	CTCAGGAGGG	CTCCGCCTTC	AATCCCACCC	GCTAAAGTAC	2280
TTGGAGCGGT	CTCTCCCTCC	CTCATCAGCC	CACCAAACCA	AACCTAGCCT	CCAAGAGTGG	2340
GAAGAAATTA	AAGCAAGATA	GGCTATTAAG	TGCAGAGGGA	GAGAAAATGC	CTCCAACATG	2400
TGAGGAAGTA	ATGAGAGAAA	TCATAGAATT	TCTTCCGCTT	CCTCGCTCAC	TGACTCGCTG	2460
CGCTCGGTG	TTCCGGCTGCG	GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	AATACGGTGA	2520
TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC	2580
AGGAACCGTA	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	CCCTGACGAG	2640
CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	CGACAGGACT	ATAAAGATAC	2700
CAGGCGTTTC	CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	GCCGCTTACC	2760
GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	AGCGTGCGCG	TTTCTCAATG	CTCACGCTGT	2820
AGGTATCTCA	GTTCCGGTGA	GGTCGTTTCG	TCCAAGCTGG	GCTGTGTGCA	CGAACCCCCC	2880
GTTTCAGCCG	ACCCTGCGCG	CTTATCCGGT	AACATATCGT	TTGAGTCCAA	CCCGGTAAGA	2940
CACGACTTAT	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	GAGGTATGTA	3000
GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	CCTAACTACG	GCTACACTAG	AAGGACAGTA	3060
TTTGGTATCT	GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	TAGCTCTTGA	3120
TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTT	TTTGCAAGCA	GCAGATTACG	3180

CGCAGAAAAA	AAGGATCTCA	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC	TGACGCTCAG	3240
TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	TATCAAAAAG	GATCTTCACC	3300
TAGATCCTTT	TAAATTAAAA	ATGAAGTTTT	AAATCAATCT	AAAGTATATA	TGAGTAAACT	3360
TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	TCTCAGCGAT	CTGTCTATTT	3420
CGTTTCATCCA	TAGTTGCCTG	ACTCCGGGGG	GGGGGGGCGC	TGAGGTCTGC	CTCGTGAAGA	3480
AGGTGTTGCT	GACTCATACC	AGGCCTGAAT	CGCCCCATCA	TCCAGCCAGA	AAGTGAGGGA	3540
GCCACGGTTG	ATGAGAGCTT	TGTTGTAGGT	GGACCAGTTG	GTGATTTTGA	ACTTTTGCTT	3600
TGCCACGGAA	CGGTCTGCGT	TGTCGGGAAG	ATGCGTGATC	TGATCCTTCA	ACTCAGCAAA	3660
AGTTCGATTT	ATTCAACAAA	GCCGCCGTCC	CGTCAAGTCA	GCGTAATGCT	CTGCCAGTGT	3720
TACAACCAAT	TAACCAATTG	TGATTAGAAA	AACTCATCGA	GCATCAAATG	AAACTGCAAT	3780
TTATTTCATAT	CAGGATTATC	AATACCATAT	TTTTGAAAAA	GCCGTTTCTG	TAATGAAGGA	3840
GAAAACTCAC	CGAGGCAGTT	CCATAGGATG	GCAAGATCCT	GGTATCGGTC	TGCGATTCCG	3900
ACTCGTCCAA	CATCAATACA	ACCTATTAAT	TTCCCCTCGT	CAAAAATAAG	GTATCAAGT	3960
GAGAAATCAC	CATGAGTGAC	GACTGAATCC	GGTGAGAATG	GCAAAAAGCTT	ATGCATTTCT	4020
TTCCAGACTT	GTTCAACAGG	CCAGCCATTA	CGCTCGTCAT	CAAAATCACT	CGCATCAACC	4080
AAACCGTTAT	TCATTTCGTGA	TTGCGCCTGA	GCGAGACGAA	ATACGCGATC	GCTGTTAAAA	4140
GGACAATTAC	AAACAGGAAT	CGAATGCAAC	CGGCGCAGGA	ACACTGCCAG	CGCATCAACA	4200
ATATTTTTCAC	CTGAATCAGG	ATATTCTTCT	AATACCTGGA	ATGCTGTTTT	CCCGGGGATC	4260
GCAGTGGTGA	GTAACCATGC	ATCATCAGGA	GTACGGATAA	AATGCTTGAT	GGTCGGAAGA	4320
GGCATAAATT	CCGTCAGCCA	GTTTAGTCTG	ACCATCTCAT	CTGTAACATC	ATTGGCAACG	4380
CTACCTTTGC	CATGTTTCAG	AAACAACCTCT	GGCGCATCGG	GCTTCCCATA	CAATCGATAG	4440
ATTGTGCGAC	CTGATTGCCC	GACATTATCG	CGAGCCCATT	TATACCCATA	TAAATCAGCA	4500
TCCATGTTGG	AATTTAATCG	CGGCCTCGAG	CAAGACGTTT	CCCGTTGAAT	ATGGCTCATA	4560
ACACCCCTTG	TATTACTGTT	TATGTAAGCA	GACAGTTTTA	TTGTTTCATGA	TGATATATTT	4620
TTATCTTGTG	CAATGTAACA	TCAGAGATTT	TGAGACACAA	CGTGGCTTTC	CCCCCCCCCC	4680
CATTATTGAA	GCATTTATCA	GGGTTATTGT	CTCATGAGCG	GATACATATT	TGAATGTATT	4740
TAGAAAAATA	AACAAATAGG	GGTTCCGCGC	ACATTTCCCC	GAAAAGTGCC	ACCTGACGTC	4800
TAAGAAACCA	TTATTATCAT	GACATTAACC	TATAAAAATA	GGCGTATCAC	GAGGCCCTTT	4860
CGTC						4864

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCAGAAGCA GAGCA

15

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCACCGTCCT TAGATCAAGC AGGGTTAATA ATCACTCACT GAGTGACATC AAAATCATGG 60
CGTCCCAAGG CACCAAACGG TCTTATGAAC AGATGGAAAC TGATGGGGAA CGCCAGATT 119

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: YES

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGGGGCAAA CAACAGATGG CTGGCAACTA GAAGGCACAG CAGATATTTT TTCCTTAATT 60
GTCGTAC 67

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCAGAAGCA CGCAC 15

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCAGAAGCA CAGCA 15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCTTAGATCG GAAATAAAAA CAACCAAAT GAA

33

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: YES

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCAGATCCTT ATATTCTGA AATTCTGGTC TCAGAT

36

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACCGTCCTTA GATCCAGAAG CAGAGCATTT TCTAATATCC ACAAATGAA GGCAATAATT
GTACTACTCA TGGTAGTAAC ATCCAACGCA GATCGAATCT GC

60

102

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: YES
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGCACAGCAG ATCTTTCAAT AACGTTTCTT TGTAATGGTA AC

42

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAACAGACT GTTCCTTTCC ATG

23

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: YES
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGAGTGGCAC CTTCCAGG

18

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCAAAAGCA GG

12

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGCAGAAGCG GAGC

14

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCACATGTCG ACCCGTAAAA AGGCCGCGTT GCTGG

35

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGTACAACCA TGAAGACTAT CATTGCTTTG AGC

33

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCACATAGAT CTTCAAATGC AAATGTTGCA CCTAATG

37

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTACAACCA TGAAAGCAAA ACTACTAGTC CTGTTATG

38

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCACATTCAG ATGCATATTC TACACTGCAA AG

32

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGTACAACCA TGAAGGCAAT AATTGTACTA CTCATG

36

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCACATTTAT AGACAGATGG AGCAAGAAAC ATTGTC

36

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGTACAAGAT CTACCATGCT TCTAACCGAG GTC

33

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCACATAGAT CTTCACTTGA ACCGTTGCAT CTGCAC

36

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGTACAGGAT CCACCATGTC CAACATGGAT ATTGACGGC

39

- (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCACATGGAT CCTTAATAAT CGAGGTCATC ATAATCCTC

39

- (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGTACAGGAT CCACCATGTC GCTGTTTGA GACACAATTG CC

42

- (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCACATGGAT CCTTATAGGT ATTTCTTCAC AAGAGCTG

38

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATATTGGCT	ATTGGCCATT	GCATACGTTG	TATCCATATC	ATAATATGTA	CATTTATATT	60
GGCTCATGTC	CAACATTACC	GCCATGTTGA	CATTGATTAT	TGACTAGTTA	TTAATAGTAA	120
TCAATTACGG	GGTCATTAGT	TCATAGCCCA	TATATGGAGT	TCCGCGTTAC	ATAACTTACG	180
GTAAATGGCC	CGCCTGGCTG	ACCGCCCAAC	GACCCCGGCC	CATTGACGTC	AATAATGACG	240
TATGTTCCCA	TAGTAACGCC	AATAGGGACT	TTCCATTGAC	GTCAATGGGT	GGAGTATTTA	300
CGGTAAACTG	CCCACCTGGC	AGTACATCAA	GTGTATCATA	TGCCAAGTAC	GCCCCCTATT	360
GACGTCAATG	ACGGTAAATG	GCCCGCCTGG	CATTATGCCC	AGTACATGAC	CTTATGGGAC	420
TTTCCTACTT	GGCAGTACAT	CTACGTATTA	GTCATCGCTA	TTACCATGGT	GATGCGGTTT	480
TGGCAGTACA	TCAATGGGCG	TGGATAGCGG	TTTGACTCAC	GGGGATTTCC	AAGTCTCCAC	540
CCCATTGACG	TCAATGGGAG	TTTGTFTTGG	CACCAAAATC	AACGGGACTT	TCCAAAATGT	600
CGTAACAAC	CCGCCCCATT	GACGCAAATG	GGCGGTAGGC	GTGTACGGTG	GGAGGTCTAT	660
ATAAGCAGAG	CTCGTTTAGT	GAACCGTCAG	ATCGCCTGGA	GACGCCATCC	ACGCTGTTTT	720
GACCTCCATA	GAAGACACCG	GGACCGATCC	AGCCTCCGCG	GCCGGGAACG	GTGCATTGGA	780
ACGCGGATTC	CCCGTGCCAA	GAGTGACGTA	AGTACCGCCT	ATAGAGTCTA	TAGGCCCCACC	840
CCCTTGGCTT	CTTATGCATG	CTATACTGTT	TTTGGCTTGG	GGTCTATACA	CCCCCGCTTC	900
CTCATGTTAT	AGGTGATGGT	ATAGCTTAGC	CTATAGGTGT	GGGTTATTGA	CCATTATTGA	960
CCACTCCCCT	ATTGGTGACG	ATACTTTCCA	TTACTAATCC	ATAACATGGC	TCTTTGCCAC	1020
AACTCTCTTT	ATTGGCTATA	TGCCAATACA	CTGTCCTTCA	GAGACTGACA	CGGACTCTGT	1080
ATTTTTACAG	GATGGGGTCT	CATTTATTAT	TTACAAATTC	ACATATACAA	CACCACCGTC	1140
CCCATGCCCC	GCAGTTTATA	TTAAACATGT	TAACGTGGGA	TCTCCACGCG	AACTCTCGGGT	1200
ACGTGTTCCG	GACATGGGCT	CTTCTCCGGT	AGCGGCGGAG	CTTCTACATC	CGAGCCCTGC	1260
TCCCATGCCT	CCAGCGACTC	ATGGTCGCTC	GGCAGCTCCT	TGCTCCTAAC	AGTGGAGGCC	1320
AGACTTAGGC	ACAGCACGAT	GCCCACCACC	ACCAGTGTGC	CGCACAAGGC	CGTGGCGGTA	1380
GGGTATGTGT	CTGAAAATGA	GCTCGGGGAG	CGGGCTTGCA	CCGCTGACGC	ATTTGGAAGA	1440
CTTAAGGCAG	CGGCAGAAGA	AGATGCAGGC	AGCTGAGTTG	TTGTGTTCTG	ATAAGAGTCA	1500
GAGGTAATC	CCGTTGCGGT	GCTGTTAACG	GTGGAGGGCA	GTGTAGTCTG	AGCAGTACTC	1560
GTTGCTGCCG	CGCGCGCCAC	CAGACATAAT	AGCTGACAGA	CTAACAGACT	GTTCTCTTCC	1620
ATGGGTCTTT	TCTGCAGTCA	CCGTCCCTAG	ATCTGCTGTG	CCTTCTAGTT	GCCAGCCATC	1680
TGTTGTTTTG	CCCTCCCCCG	TGCCTTCCTT	GACCCGTGAA	GGTGCCACTC	CCACTGTCCT	1740
TTCCTAATAA	AATGAGGAAA	TTGCATCGCA	TTGTCTGAGT	AGGTGTCATT	CTATTCTGGG	1800
GGGTGGGGTG	GGGCAGCACA	GCAAGGGGGA	GGATTGGGAA	GACAATAGCA	GGCATGCTGG	1860
GGATGCGGTG	GGCTCTATGG	GTACGCGCCG	AGCGGCCGTA	CCCAGGTGCT	GAAGAATTGA	1920
CCCGGTTTCT	CGACCCGTAA	AAAGGCCGCG	TTGCTGGCGT	TTTTCCATAG	GCTCCGCCCC	1980
CCTGACGAGC	ATCACAAAAA	TCGACGCTCA	AGTCAGAGGT	GGCGAAACCC	GACAGCTACTA	2040
TAAAGATACC	AGGCGTTTCC	CCCTGGAAGC	TCCCTCGTGC	GCTCTCCTGT	TCCGACCCTG	2100
CCGCTTACCG	GATACCTGTC	CGCCTTTCTC	CCTTCGGGAA	GCGTGCGCCT	TTCTCAATGC	2160
TCACGCTGTA	GGTATCTCAG	TTCCGGTGTA	GTCGTTTCGT	CCAAGCTGGG	CTGTGTGCAC	2220
GAACCCCGCG	TTACACCCGA	CCGCTGCGGC	TTATCCGGTA	ACTATCGTCT	TGAGTCCAAC	2280
CCGGTAAGAC	ACGACTTATC	GCCACTGGCA	GCAGCCACTG	GTAACAGGAT	TAGCAGAGCG	2340
AGGTATGTAG	GCGGTGCTAC	AGAGTTCTTG	AAGTGGTGGC	CTAACTACGG	CTACACTAGC	2400
TGAAGGACAG	TATTTGGTAT	CTGCGCTCTG	CTGAAGCCAG	TTACCTTCGG	AAAAAGAGTT	2460

GGTAGCTCTT	GATCCGGCAA	ACAAACCACC	GCTGGTAGCG	GTGGTTTTTT	TGTTTGCAAG	2520
CAGCAGATTA	CGCGCAGAAA	AAAAGGATCT	CAAGAAGATC	CTTTGATCTT	TTCTACGTGA	2580
TCCCGTAATG	CTCTGCCAGT	GTTACAACCA	ATTAACCAAT	TCTGATTAGA	AAAACATCATC	2640
GAGCATCAAA	TGAAACTGCA	ATTTATTTCAT	ATCAGGATTA	TCAATACCAT	ATTTTTGAAA	2700
AAGCCGTTTC	TGTAATGAAG	GAGAAAACTC	ACCGAGGCAG	TTCCATAGGA	TGGCAAGATC	2760
CTGGTATCGG	TCTGCGATT	CGACTCGTCC	AACATCAATA	CAACCTATTA	ATTTCCCTC	2820
GTCAAAAATA	AGGTTATCAA	GTGAGAAATC	ACCATGAGTG	ACGACTGAAT	CCGGTGAGAA	2880
TGGCAAAAGC	TTATGCATTT	CTTTCCAGAC	TTGTTCAACA	GGCCAGCCAT	TACGCTCGTC	2940
ATCAAAATCA	CTCGCATCAA	CCAAACCGTT	ATTCATTCGT	GATTGCGCCT	GAGCGAGACG	3000
AAATACGCGA	TCGCTGTTAA	AAGGACAATT	ACAAACAGGA	ATCGAATGCA	ACCGGCGCAG	3060
GAACACTGCC	AGCGCATCAA	CAATATTTTC	ACCTGAATCA	GGATATTCCT	CTAATACCTG	3120
GAATGCTGTT	TTCCCGGGGA	TCGCAGTGGT	GAGTAACCAT	GCATCATCAG	GAGTACGGAT	3180
AAAATGCTTG	ATGGTCGGAA	GAGGCATAAA	TTCCGTCAGC	CAGTTTAGTC	TGACCATCTC	3240
ATCTGTAAAC	TCATTGGCAA	CGCTACCTTT	GCCATGTTTC	AGAAACAAC	CTGGCGCATC	3300
GGGCTTCCCA	TACAATCGAT	AGATTGTCGC	ACCTGATTGC	CCGACATTAT	CGCGAGCCCA	3360
TTTATACCCA	TATAAATCAG	CATCCATGTT	GGAATTTAAT	CGCGGCCTCG	AGCAAGACGT	3420
TTCCCGTTGA	ATATGGCTCA	TAACACCCCT	TGTATTACTG	TTATGTAAAG	CAGACAGTTT	3480
TATTGTTTCAT	GATGATATAT	TTTTATCTTG	TGCAATGTAA	CATCAGAGAT	TTTGAGACAC	3540
AACGTGGCTT	TCC					3553

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCACCGTCCT	TAGATCGGTA	CAACCATGAA	GACTATCATT	GCTTTGAGCT	ACATTTTATG	60
TCTGGTTTTT	GC					72

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCATGCTTTT	TGCTTTGTGT	TGTTTTGCTG	GGGTTTCATCA	TGTGGGCCTG	CCAAAAAGGC	60
AACATTAGGT	GCAACATTTG	CATTTGAAGA	TCTATGTGGG	ATCTGCTGTG	C	111

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TTAGATCGGA ACATGAAAGC AAAACTACTA GTCCTGTTAT GTGCATTAC AGCTACATAT 60
GCA 63

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTGGTGCTTT TGGTCTCCCT GGGGGCAATC AGCTTCTGGA TGTGTTCTAA TGGGTCTTTG 60
CAGTGTAGAA TATGCATCTG AATGTGGGAT CTGCTGTGCC TT 102

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CCTTAGATCG GTACAACCAT GAAGGCAATA ATTGTACTAC TCATGGTAGT AACATCCAAC 60
GCAGATCGAA TCTGCACTGG GATAACATCT TCAAATCAC CTCATGTG 108

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTGGCTGTAA CATTGATGAT AGCTATTTTT ATTGTTTATA TGGTCTCCAG AGACAATGTT 60
 TCTTGCTCCA TCTGTCTATA AATGTGGGAT CTGCTGTGCC TT 102

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTCCTTAGAT CCACCATGGC GTCCCAAGGC ACCAAACGGT CTTATGAACA GATGGAAACT 60
 GATGGGGAAC GCCAGAATGC AACT 84

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAAAAGGCAA CGAACCCGAT CGTGCCCTCT TTTGACATGA GTAATGAAGG ATCTTATTTT 60
 TTCGGAGACA ATGCAGAAGA GTACGACAAT TAAGGATCTG CTGTGCCT 108

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTTAGATCCA	GATCTACCAT	GAGTCTTCTA	ACCGAGGTCG	AAACGTATGT	TCTCTCTATC	60
GTTCCATCAG	GCCCCCTCAA	AGCCGAAATC	GCGCAGAGAC	TTGAAGATGT	CTTTGCTGGG	120
AAAAACACAG	AT					132

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGGACTCATC	CTAGCTCCAG	TACTGGTCTA	AAAGATGATC	TTCTTGAAAA	TTTGCAGACC	60
TATCAGAAAC	GAATGGGGGT	GCAGATGCAA	CGGTTCAAGT	GAAGATCTAT	GTGGGATCTG	120
CTGTGCCTT						129

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTTAGATCCA	CCATGTCCAA	CATGGATATT	GACGGTATCA	ACACTGGGAC	AATTGACAAA	60
ACACCGGAAG	AAATAACTTC	T				81

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTTGAAATTC	CAATTAAGCA	GACCATCCCC	AATTTCTTCT	TTGGGAGGGA	CACAGCAGAG	60
------------	------------	------------	------------	------------	------------	----

GATTATGATG ACCTCGATTA TTAAGGATCT GCTGTG

96

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTTAGATCCA CCATGTCGCT GTTTGGAGAC ACAATTGCCT ACCTGCTTTC ATTGACAGAA	60
GATGGAGAAG GCAAAGCAGA ACTAGCAGAA AAATTA	96

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGATCTCTTG GGGCAAGTCA AGAGAAATGGG GAAGGAATTG CAAAGGATGT GATGGAAGTG	60
CTAAAGCAGA GCTCTATGGG AAATTCAGCT CTTGTGAAGA AATACCTATA AGGATCTGCT	120
GTG	123

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGTACAAATA TTGGCTATTG GCCATTGCAT ACG	33
--------------------------------------	----

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCACATCTCG AGGAACCGGG TCAATTCTTC AGCACC

36

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGTACAGATA TCGGAAAGCC ACGTTGTGTC TCAAAATC

38

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCACATGGAT CCGTAATGCT CTGCCAGTGT TACAACC

37

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGTACATGAT CACGTAGAAA AGATCAAAGG ATCTTCTTG

39